

0280

42

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/006,191

DATE: 12/14/2001

TIME: 10:30:19

Input Set : A:\RTS-0274 Sequence Listing.txt

Output Set: N:\CRF3\12142001\I006191.raw

ENTERED

6 <110> APPLICANT: William Gaarde

7 Andrew T. Watt

9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR

EXPRESSION

11 <130> FILE REFERENCE: RTS-0274

C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/006,191

C--> 13 <141> CURRENT FILING DATE: 2001-12-10

13 <160> NUMBER OF SEQ ID NOS: 153

16 <210> SEQ ID NO: 1

17 <211> LENGTH: 20

18 <212> TYPE: DNA

19 <213> ORGANISM: Artificial Sequence

21 <220> FEATURE:

23 <223> OTHER INFORMATION: Antisense Oligonucleotide

25 <400> SEQUENCE: 1

26 tccgtcatcg ctcctcaggg

20

29 <210> SEQ ID NO: 2

30 <211> LENGTH: 20

31 <212> TYPE: DNA

32 <213> ORGANISM: Artificial Sequence

34 <220> FEATURE:

36 <223> OTHER INFORMATION: Antisense Oligonucleotide

38 <400> SEQUENCE: 2

39 atgcattctg cccccaagga

20

41 <210> SEQ ID NO: 3

42 <211> LENGTH: 2075

43 <212> TYPE: DNA

44 <213> ORGANISM: Homo sapiens

46 <220> FEATURE:

48 <221> NAME/KEY: CDS

49 <222> LOCATION: (130)...(1179)

51 <400> SEQUENCE: 3

52 cccggccgac agccccgaga cgacagcccg gcgcgtcccg gtccccacct ccgaccaccg 60

53 ccagcgctcc aggccccgcg ctccccgctc gcgcgcaccg cgccctccgc tccgccccga 120

54 gtgccaacc atg acc gcc gcc agt atg ggc ccc gtc cgc gtc gcc ttc gtg 171

55 Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val

56 1 5 10

58 gtc ctc ctc gcc ctc tgc agc cgg ccg gcc gtc ggc cag aac tgc agc 219

59 Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser

60 15 20 25 30

62 ggg ccg tgc cgg tgc ccg gac gag ccg gcg ccg cgc tgc ccg gcg ggc 267

63 Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly

64 35 40 45

66 gtg agc ctc gtg ctg gac ggc tgc ggc tgc tgc cgc gtc tgc gcc aag 315

67 Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys

68 50 55 60

70 cag ctg ggc gag ctg tgc acc gag cgc gac ccc tgc gac ccg cac aag 363

71 Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys

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72	65	70	75	
74	ggc ctc ttc tgt gac ttc ggc tcc ccg gcc aac cgc aag atc ggc gtg	411		
75	Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val			
76	80	85	90	
78	tgc acc gcc aaa gat ggt gct ccc tgc atc ttc ggt ggt acg gtg tac	459		
79	Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr			
80	95	100	105	110
82	cgc agc gga gag tcc ttc cag agc agc tgc aag tac cag tgc acg tgc	507		
83	Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys			
84	115	120	125	
86	ctg gac ggg gcg gtg ggc tgc atg ccc ctg tgc agc atg gac gtt cgt	555		
87	Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg			
88	130	135	140	
90	ctg ccc agc cct gac tgc ccc ttc ccg agg agg gtc aag ctg ccc ggg	603		
91	Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly			
92	145	150	155	
94	aaa tgc tgc gag gag tgg gtg tgt gac gag ccc aag gac caa acc gtg	651		
95	Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val			
96	160	165	170	
98	gtt ggg cct gcc ctc gcg gct tac cga ctg gaa gac acg ttt ggc cca	699		
99	Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro			
100	175	180	185	190
102	gac cca act atg att aga gcc aac tgc ctg gtc cag acc aca gag tgg	747		
103	Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp			
104	195	200	205	
106	agc gcc tgt tcc aag acc tgt ggg atg ggc atc tcc acc cgg gtt acc	795		
107	Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr			
108	210	215	220	
110	aat gac aac gcc tcc tgc agg cta gag aag cag agc cgc ctg tgc atg	843		
111	Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met			
112	225	230	235	
114	gtc agg cct tgc gaa gct gac ctg gaa gag aac att aag aag ggc aaa	891		
115	Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys			
116	240	245	250	
118	aag tgc atc cgt act ccc aaa atc tcc aag cct atc aag ttt gag ctt	939		
119	Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu			
120	255	260	265	270
122	tct ggc tgc acc agc atg aag aca tac cga gct aaa ttc tgt gga gta	987		
123	Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val			
124	275	280	285	
126	tgt acc gac ggc cga tgc tgc acc ccc cac aga acc acc acc ctg ccg	1035		
127	Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro			
128	290	295	300	
130	gtg gag ttc aag tgc cct gac ggc gag gtc atg aag aag aac atg atg	1083		
131	Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met			
132	305	310	315	
134	ttc atc aag acc tgt gcc tgc cat tac aac tgt ccc gga gac aat gac	1131		
135	Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp			
136	320	325	330	

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```

138 atc ttt gaa tcg ctg tac tac agg aag atg tac gga gac atg gca tga 1179
139 Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala *
140 335 340 345
142 agccagagag tgagagacat taactcatta gactggaact tgaactgatt cacatctcat 1239
143 ttttccgtaa aaatgatttc agtagcaciaa gttattttaa tctgtttttc taactggggg 1299
144 aaaagattcc caccacattc aaaacattgt gccatgtcaa acaaatagtc tatcttcccc 1359
145 agacactggt ttgaagaatg ttaagacttg acagtgggagc tacattagta cacagcacca 1419
146 gaatgtatat taagggtgtg ctttaggagc agtgggaggg taccggcccg gttagtatca 1479
147 tcagatcgac tcttatacga gtaatatgcc tgctatttga agtgtaattg agaaggaaaa 1539
148 ttttagcgtg ctactgacc tgctgtagc cccagtgaca gctaggatgt gcattctcca 1599
149 gccatcaaga gactgagtc agttgttct taagtcagaa cagcagactc agctctgaca 1659
150 ttctgattcg aatgacactg ttcaggaatc ggaatcctgt cgattagact ggacagcttg 1719
151 tggcaagtga atttgctgt aacaagccag atttttttaa atttatattg taaatattgt 1779
152 gtgtgtgtgt gtgtgtgtat atatatatat atatgtacag ttatctaagt taatttaaag 1839
153 ttgtttgtgc ctttttattt ttgtttttaa tgctttgata ttcaatgtt agcctcaatt 1899
154 tctgaacacc ataggtagaa tgtaaagctt gtctgatcgt tcaaagcatg aaatggatac 1959
155 ttatatggaa attctgctca gatagaatga cagtcocgtca aaacagattg tttgcaaagg 2019
156 ggagcatca gtgtcttggc aggctgattt ctaggtagga aatgtggtag ctacag 2075
159 <210> SEQ ID NO: 4
160 <211> LENGTH: 22
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
166 <223> OTHER INFORMATION: PCR Primer
168 <400> SEQUENCE: 4
169 acaagggcct cttctgtgac tt 22
172 <210> SEQ ID NO: 5
173 <211> LENGTH: 22
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
179 <223> OTHER INFORMATION: PCR Primer
181 <400> SEQUENCE: 5
182 ggtacaccgt accaccgaag at 22
185 <210> SEQ ID NO: 6
186 <211> LENGTH: 23
187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
192 <223> OTHER INFORMATION: PCR Probe
194 <400> SEQUENCE: 6
195 tgtgcaccgc caaagatggt gct 23
198 <210> SEQ ID NO: 7
199 <211> LENGTH: 19
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
205 <223> OTHER INFORMATION: PCR Primer
207 <400> SEQUENCE: 7

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208 gaaggtgaag gtcggagtc 19
211 <210> SEQ ID NO: 8
212 <211> LENGTH: 20
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
218 <223> OTHER INFORMATION: PCR Primer
220 <400> SEQUENCE: 8
221 gaagatggtg atgggatttc 20
224 <210> SEQ ID NO: 9
225 <211> LENGTH: 20
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
231 <223> OTHER INFORMATION: PCR Probe
233 <400> SEQUENCE: 9
234 caagcttccc gttctcagcc 20
237 <210> SEQ ID NO: 10
238 <211> LENGTH: 2334
239 <212> TYPE: DNA
240 <213> ORGANISM: Mus musculus
242 <220> FEATURE:
244 <221> NAME/KEY: CDS
245 <222> LOCATION: (206)...(1252)
247 <400> SEQUENCE: 10
248 gaagactcag ccagatccac tccagctccg accccaggag accgacctcc tccagacggc 60
249 agcagcccca gccagccga caacccaga cgccaccgcc tggagcggtcc agacaccaac 120
250 ctccgcccct gtccgaatcc aggtccggc cgcgcctctc gtcgcctctg caccctgctg 180
251 tgcacctcc taccgcgtcc cgatc atg ctc gcc tcc gtc gca ggt ccc atc 232
252 Met Leu Ala Ser Val Ala Gly Pro Ile
253 1 5
255 agc ctc gcc ttg gtg ctc ctc gcc ctc tgc acc cgg cct gct acg ggc 280
256 Ser Leu Ala Leu Val Leu Leu Ala Leu Cys Thr Arg Pro Ala Thr Gly
257 10 15 20 25
259 cag gac tgc agc gcg caa tgt cag tgc gca gcc gaa gca gcg ccg cac 328
260 Gln Asp Cys Ser Ala Gln Cys Gln Cys Ala Ala Glu Ala Ala Pro His
261 30 35 40
263 tgc ccc gcc ggc gtg agc ctg gtg ctg gac ggc tgc ggc tgc tgc cgc 376
264 Cys Pro Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg
265 45 50 55
267 gtc tgc gcc aag cag ctg gga gaa ctg tgt acg gag cgt gac ccc tgc 424
268 Val Cys Ala Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys
269 60 65 70
271 gac cca cac aag ggc ctc ttc tgc gat ttc ggc tcc ccc gcc aac cgc 472
272 Asp Pro His Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg
273 75 80 85
275 aag atc gga gtg tgc act gcc aaa gat ggt gca ccc tgt gtc ttc ggt 520
276 Lys Ile Gly Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Val Phe Gly
277 90 95 100 105

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279 ggg tcg gtg tac cgc agc ggt gag tcc ttc caa agc agc tgc aaa tac 568
280 Gly Ser Val Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr
281      110      115      120
283 caa tgc act tgc ctg gat ggg gcc gtg ggc tgc gtg ccc ctg tgc agc 616
284 Gln Cys Thr Cys Leu Asp Gly Ala Val Gly Cys Val Pro Leu Cys Ser
285      125      130      135
287 atg gac gtg cgc ctg ccc agc cct gac tgc ccc ttc ccg aga agg gtc 664
288 Met Asp Val Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val
289      140      145      150
291 aag ctg cct ggg aaa tgc tgc gag gag tgg gtg tgt gac gag ccc aag 712
292 Lys Leu Pro Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys
293      155      160      165
295 gac cgc aca gca gtt ggc cct gcc cta gct gcc tac cga ctg gaa gac 760
296 Asp Arg Thr Ala Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp
297 170      175      180      185
299 aca ttt ggc cca gac cca act atg atg cga gcc aac tgc ctg gtc cag 808
300 Thr Phe Gly Pro Asp Pro Thr Met Met Arg Ala Asn Cys Leu Val Gln
301      190      195      200
303 acc aca gag tgg agc gcc tgt tct aag acc tgt ggg atg ggc atc tcc 856
304 Thr Thr Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser
305      205      210      215
307 acc cga gtt acc aat gac aat acc ttc tgc aga ctt gag aag cag agt 904
308 Thr Arg Val Thr Asn Asp Asn Thr Phe Cys Arg Leu Glu Lys Gln Ser
309      220      225      230
311 cgc ctc tgc atg gtc agg ccc tgc gaa gct gac ctg gag gaa aac att 952
312 Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile
313      235      240      245
315 aag aag ggc aaa aag tgc atc cgg aca cct aaa atc gcc aag cct gtc 1000
316 Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ala Lys Pro Val
317 250      255      260      265
319 aag ttt gag ctt tct ggc tgc acc agt gtg aag aca tac agg gct aag 1048
320 Lys Phe Glu Leu Ser Gly Cys Thr Ser Val Lys Thr Tyr Arg Ala Lys
321      270      275      280
323 ttc tgc ggg gtg tgc aca gac ggc cgc tgc tgc aca ccg cac aga acc 1096
324 Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr
325      285      290      295
327 acc act ctg cca gtg gag ttc aaa tgc ccc gat ggc gag atc atg aaa 1144
328 Thr Thr Leu Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Ile Met Lys
329      300      305      310
331 aag aat atg atg ttc atc aag acc tgt gcc tgc cat tac aac tgt cct 1192
332 Lys Asn Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro
333      315      320      325
335 ggg gac aat gac atc ttt gag tcc ctg tac tac agg aag atg tac gga 1240
336 Gly Asp Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly
337 330      335      340      345
339 gac atg gcg taa agccaggaag taaggagacac gaactcatta gactataact 1292
340 Asp Met Ala *
343 tgaactgagt tgcattctcat tttcttctgt aaaaacaatt acagtagcac attaatTTaa 1352
344 atctgtgttt ttaactaccg tgggaggaac tatccacca aagtgagaac gttatgtcat 1412

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/006,191

DATE: 12/14/2001

TIME: 10:30:21

Input Set : A:\RTS-0274 Sequence Listing.txt

Output Set: N:\CRF3\12142001\I006191.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date